

A. Nelson

RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

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21

APR 27 2001

RECEIVED

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/446,089B

Source: 1638

Date Processed by STIC: 4-17-01

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FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

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Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

1638

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/446,089B

DATE: 04/17/2001
TIME: 13:33:07

Input Set : A:\001560-377.ST25.txt
Output Set: N:\CRF3\04172001\I446089B.raw

Does Not Comply
Corrected Diskette Needed
see p. 6

3 <110> APPLICANT: SAKAKIBARA, Keiko
4 FUKUI, Yuko
5 TANAKA, Yoshikazu
6 KUSUMI, Takaaki
7 MIZUTANI, Masako
8 NAKAYAMA, Toru
10 <120> TITLE OF INVENTION: GENE ENCODING PROTEIN HAVING AURONE SYNTHESIZING ACTIVITY
12 <130> FILE REFERENCE: 001560-377
14 <140> CURRENT APPLICATION NUMBER: US 09/446,089B
15 <141> CURRENT FILING DATE: 1999-12-17
17 <150> PRIOR APPLICATION NUMBER: PCT/JP99/02045
18 <151> PRIOR FILING DATE: 1999-04-16
20 <150> PRIOR APPLICATION NUMBER: JP 10/107296
21 <151> PRIOR FILING DATE: 1998-04-17
23 <160> NUMBER OF SEQ ID NOS: 15
25 <170> SOFTWARE: PatentIn version 3.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 1951
30 <212> TYPE: DNA
31 <213> ORGANISM: Antirrhinum majus
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (96)..(1781)
37 <400> SEQUENCE: 1
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40 gttgtttatt atcaatcaaa taaaattatt tccca atg ttc aaa aat cct aat 113
41 Met Phe Lys Asn Pro Asn
42 1 5
44 atc cgc tat cac aaa cta tot tcc aaa tcc aat gac aac gat caa gaa 161
45 Ile Arg Tyr His Lys Leu Ser Ser Lys Ser Asn Asp Asn Asp Gln Glu
46 10 15 20
48 tcc tcc cat cgt tgt aag cac att cta tta ttt ata ata acc tta ttc 209
49 Ser Ser His Arg Cys Lys His Ile Leu Leu Phe Ile Ile Thr Leu Phe
50 25 30 35
52 cta ctt ata gtt ggc ctg tac atc gcc aac tct ctc gcc tat gcc cgg 257
53 Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn Ser Leu Ala Tyr Ala Arg
54 40 45 50
56 ttt gcc tcg acc tca acc ggc cct atc gcc gcc cct gat gtc acc aaa 305
57 Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala Ala Pro Asp Val Thr Lys
58 55 60 65 70
60 tgt ggt cag cca gac ttg cca cct ggc aca gcc cca ata aac tgt tgt 353
61 Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr Ala Pro Ile Asn Cys Cys
62 75 80 85
64 ccc cca atc ccc gct aaa atc atc gat ttc gag cta cca cct ccc tcc 401
65 Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe Glu Leu Pro Pro Pro Ser
66 90 95 100
68 act acc atg agg gtt cgc cgt gcg gct cat tta gtt gat gat gca tac 449

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DATE: 04/17/2001

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TIME: 13:33:07

Input Set : A:\001560-377.ST25.txt

Output Set: N:\CRF3\04172001\I446089B.raw

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69 Thr Thr Met Arg Val Arg Arg Ala Ala His Leu Val Asp Asp Ala Tyr
70      105      110      115
72 att gcc aaa ttc aag aaa gcc gtt gag ctt atg cga gct cta cct gag      497
73 Ile Ala Lys Phe Lys Lys Ala Val Glu Leu Met Arg Ala Leu Pro Glu
74      120      125      130
76 gat gac cct cgt agc ttc aag caa caa gct aac gtc cat tgc gct tac      545
77 Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala Asn Val His Cys Ala Tyr
78 135      140      145      150
80 tgc gcg ggg gcg tat aat caa gcc ggt ttc aca aac cta aag ctc caa      593
81 Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe Thr Asn Leu Lys Leu Gln
82      155      160      165
84 atc cac cga tct tgg ctt ttt ttc ccg ttc cat aga tat tat atc tac      641
85 Ile His Arg Ser Trp Leu Phe Phe Pro Phe His Arg Tyr Tyr Ile Tyr
86      170      175      180
88 ttt ttt gaa aga ata ttg gga aaa cta atc aat gat aca act ttt gct      689
89 Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile Asn Asp Thr Thr Phe Ala
90      185      190      195
92 ctc caa ttt tgg aac tat gat tca cct ggt gga atg aca atc cca tca      737
93 Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly Gly Met Thr Ile Pro Ser
94      200      205      210
96 atg ttt att gat act aat tct tcg ctg tac gat agt tta cgg gac agt      785
97 Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr Asp Ser Leu Arg Asp Ser
98 215      220      225      230
100 aat cat cag cca cca acc atc gta gac ttg aac tac gcc ttt tct gat      833
101 Asn His Gln Pro Pro Thr Ile Val Asp Leu Asn Tyr Ala Phe Ser Asp
102      235      240      245
104 tcc gac aat acc act act cct gaa gag caa atg att ata aac ctt aaa      881
105 Ser Asp Asn Thr Thr Thr Pro Glu Glu Met Ile Ile Asn Leu Lys
106      250      255      260
108 att gtg tac aga caa atg gtg tcg agc gct aag act cca cag ctt ttc      929
109 Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys Thr Pro Gln Leu Phe
110      265      270      275
112 ttc ggc cgc cca tac cga cgt ggg gac caa gag ttt ccc ggg gtg ggg      977
113 Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln Glu Phe Pro Gly Val Gly
114      280      285      290
116 tcg att gag tta gtc cct cat ggc atg ata cat tta tgg acc ggt tct      1025
117 Ser Ile Glu Leu Val Pro His Gly Met Ile His Leu Trp Thr Gly Ser
118 295      300      305      310
120 gag aac acg ccc tat ggc gag aac atg ggg gct ttc tac tca acg gct      1073
121 Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly Ala Phe Tyr Ser Thr Ala
122      315      320      325
124 aga gac ccg ata ttt ttt gct cat cat tcg aac gtc gat aga atg tgg      1121
125 Arg Asp Pro Ile Phe Phe Ala His His Ser Asn Val Asp Arg Met Trp
126      330      335      340
128 tcc ata tgg aag acc cta gga ggg ccg cgg agg acg gac tta aca gat      1169
129 Ser Ile Trp Lys Thr Leu Gly Gly Pro Arg Arg Thr Asp Leu Thr Asp
130      345      350      355
132 cca gat ttt ctt gat gcg tct ttc gtt ttt tat gac gaa aac gca gag      1217
133 Pro Asp Phe Leu Asp Ala Ser Phe Val Phe Tyr Asp Glu Asn Ala Glu

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134      360      365      370
136 atg gtt cgg gtc aag gtt cgg gat tgc tta gat gaa aag aaa cta ggg 1265
137 Met Val Arg Val Lys Val Arg Asp Cys Leu Asp Glu Lys Lys Leu Gly
138 375      380      385      390
140 tac gtt tat caa gat gtg gag att ccg tgg ctc aac act cgt cca aca 1313
141 Tyr Val Tyr Gln Asp Val Glu Ile Pro Trp Leu Asn Thr Arg Pro Thr
142      395      400      405
144 cca aaa gtt tct cgg tct cta ctt aag aaa ttt cat aga aca aac act 1361
145 Pro Lys Val Ser Pro Ser Leu Leu Lys Lys Phe His Arg Thr Asn Thr
146      410      415      420
148 gcc aat cgg aga caa gtt ttt cct gcg ata ctt gac aga gtc tta aaa 1409
149 Ala Asn Pro Arg Gln Val Phe Pro Ala Ile Leu Asp Arg Val Leu Lys
150      425      430      435
152 gtt atc gtg acg agg ccg aag aaa act aga agt agg aaa gaa aag gac 1457
153 Val Ile Val Thr Arg Pro Lys Lys Thr Arg Ser Arg Lys Glu Lys Asp
154      440      445      450
156 gag tta gaa gag att tta gtg att gaa ggg att gaa ctg gaa aga gac 1505
157 Glu Leu Glu Glu Ile Leu Val Ile Glu Gly Ile Glu Leu Glu Arg Asp
158 455      460      465      470
160 cac ggg cac gta aaa ttc gac gtt tat att aat gct gac gaa gat gac 1553
161 His Gly His Val Lys Phe Asp Val Tyr Ile Asn Ala Asp Glu Asp Asp
162      475      480      485
164 ctt gcg gtg att tcg ccg gag aat gct gag ttc gcc ggg agt ttc gtg 1601
165 Leu Ala Val Ile Ser Pro Glu Asn Ala Glu Phe Ala Gly Ser Phe Val
166      490      495      500
168 agt ctg tgg cac aaa cct ata aag ggg aag agg aca aag acg cag tta 1649
169 Ser Leu Trp His Lys Pro Ile Lys Gly Lys Arg Thr Lys Thr Gln Leu
170      505      510      515
172 tta aca ttg tcg att tgt gat att ttg gag gat ttg gat gct gac gaa 1697
173 Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu Asp Leu Asp Ala Asp Glu
174      520      525      530
176 gat gat tat gtg ttg gtc act ttg gtt ccg aga aac gcc gga gat gcg 1745
177 Asp Asp Tyr Val Leu Val Thr Leu Val Pro Arg Asn Ala Gly Asp Ala
178 535      540      545      550
180 atc aag att cat aat gtc aag att gag ctt gat ggc'taataaattc 1791
181 Ile Lys Ile His Asn Val Lys Ile Glu Leu Asp Gly
182      555      560
184 tattgatttc ttctcaacct acagttgatc atttacgat tgattattcc aataaaagta 1851
186 tctcatgtac caatatcgat cgtattaatc gtaatacttt cagattttta tttatttaaa 1911
188 agcagttgta taaatggtga aataaggatt actttttgag 1951
191 <210> SEQ ID NO: 2
192 <211> LENGTH: 562
193 <212> TYPE: PRT
194 <213> ORGANISM: Antirrhinum majus
196 <400> SEQUENCE: 2
198 Met Phe Lys Asn Pro Asn Ile Arg Tyr His Lys Leu Ser Ser Lys Ser
199 1      5      10      15
202 Asn Asp Asn Asp Gln Glu Ser Ser His Arg Cys Lys His Ile Leu Leu
203      20      25      30

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206 Phe Ile Ile Thr Leu Phe Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn
207          35          40          45
210 Ser Leu Ala Tyr Ala Arg Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala
211          50          55          60
214 Ala Pro Asp Val Thr Lys Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr
215 65          70          75          80
218 Ala Pro Ile Asn Cys Cys Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe
219          85          90          95
222 Glu Leu Pro Pro Pro Ser Thr Thr Met Arg Val Arg Arg Ala Ala His
223          100          105          110
226 Leu Val Asp Asp Ala Tyr Ile Ala Lys Phe Lys Lys Ala Val Glu Leu
227          115          120          125
230 Met Arg Ala Leu Pro Glu Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala
231          130          135          140
234 Asn Val His Cys Ala Tyr Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe
235 145          150          155          160
238 Thr Asn Leu Lys Leu Gln Ile His Arg Ser Trp Leu Phe Phe Pro Phe
239          165          170          175
242 His Arg Tyr Tyr Ile Tyr Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile
243          180          185          190
246 Asn Asp Thr Thr Phe Ala Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly
247          195          200          205
250 Gly Met Thr Ile Pro Ser Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr
251          210          215          220
254 Asp Ser Leu Arg Asp Ser Asn His Gln Pro Pro Thr Ile Val Asp Leu
255 225          230          235          240
258 Asn Tyr Ala Phe Ser Asp Ser Asp Asn Thr Thr Thr Pro Glu Glu Gln
259          245          250          255
262 Met Ile Ile Asn Leu Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala
263          260          265          270
266 Lys Thr Pro Gln Leu Phe Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln
267          275          280          285
270 Glu Phe Pro Gly Val Gly Ser Ile Glu Leu Val Pro His Gly Met Ile
271          290          295          300
274 His Leu Trp Thr Gly Ser Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly
275 305          310          315          320
278 Ala Phe Tyr Ser Thr Ala Arg Asp Pro Ile Phe Phe Ala His His Ser
279          325          330          335
282 Asn Val Asp Arg Met Trp Ser Ile Trp Lys Thr Leu Gly Gly Pro Arg
283          340          345          350
286 Arg Thr Asp Leu Thr Asp Pro Asp Phe Leu Asp Ala Ser Phe Val Phe
287          355          360          365
290 Tyr Asp Glu Asn Ala Glu Met Val Arg Val Lys Val Arg Asp Cys Leu
291          370          375          380
294 Asp Glu Lys Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro Trp
295 385          390          395          400
298 Leu Asn Thr Arg Pro Thr Pro Lys Val Ser Pro Ser Leu Leu Lys Lys
299          405          410          415
302 Phe His Arg Thr Asn Thr Ala Asn Pro Arg Gln Val Phe Pro Ala Ile

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RAW SEQUENCE LISTING
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DATE: 04/17/2001
TIME: 13:33:07

Input Set : A:\001560-377.ST25.txt
Output Set: N:\CRF3\04172001\I446089B.raw

```

303          420          425          430
306 Leu Asp Arg Val Leu Lys Val Ile Val Thr Arg Pro Lys Lys Thr Arg
307          435          440          445
310 Ser Arg Lys Glu Lys Asp Glu Leu Glu Glu Ile Leu Val Ile Glu Gly
311          450          455          460
314 Ile Glu Leu Glu Arg Asp His Gly His Val Lys Phe Asp Val Tyr Ile
315 465          470          475          480
318 Asn Ala Asp Glu Asp Asp Leu Ala Val Ile Ser Pro Glu Asn Ala Glu
319          485          490          495
322 Phe Ala Gly Ser Phe Val Ser Leu Trp His Lys Pro Ile Lys Gly Lys
323          500          505          510
326 Arg Thr Lys Thr Gln Leu Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu
327          515          520          525
330 Asp Leu Asp Ala Asp Glu Asp Asp Tyr Val Leu Val Thr Leu Val Pro
331          530          535          540
334 Arg Asn Ala Gly Asp Ala Ile Lys Ile His Asn Val Lys Ile Glu Leu
335 545          550          555          560
338 Asp Gly
342 <210> SEQ ID NO: 3
343 <211> LENGTH: 13
344 <212> TYPE: PRT
345 <213> ORGANISM: Antirrhinum majus
347 <400> SEQUENCE: 3
349 Lys Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro
350 1          5          10
352 <210> SEQ ID NO: 4
353 <211> LENGTH: 12
354 <212> TYPE: PRT
355 <213> ORGANISM: Antirrhinum majus
357 <400> SEQUENCE: 4
359 Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys
360 1          5          10
362 <210> SEQ ID NO: 5
363 <211> LENGTH: 18
364 <212> TYPE: PRT
365 <213> ORGANISM: Antirrhinum majus
367 <400> SEQUENCE: 5
369 Lys Thr Pro Gln Leu Phe Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln
370 1          5          10          15
372 Glu Phe
375 <210> SEQ ID NO: 6
376 <211> LENGTH: 29
377 <212> TYPE: PRT
378 <213> ORGANISM: Antirrhinum majus
380 <220> FEATURE:
381 <221> NAME/KEY: UNSURE
382 <222> LOCATION: (9)...(9)
383 <223> OTHER INFORMATION: Amino acid 9 is Xaa wherein Xaa = unknown or other.
385 <220> FEATURE:

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See p. 6

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<210> 6 Seg # 6
 <211> 29
 <212> PRT
 <213> Antirrhinum majus

<220>
 <221> UNSURE
 <222> (9)..(9) → Xaa is at position 8
 <223> Amino acid 9 is Xaa wherein Xaa = unknown or other.

<220>
 <221> UNSURE
 <222> (29)..(29) → Xaa is at position 28
 <223> Amino acid 29 is Xaa wherein Xaa = unknown or other.

<400> 6

Lys Ile Asp Phe Glu Leu Pro Xaa Pro Ser Thr Thr Met Arg Val Arg
 1 5 8 10 15

Arg Ala Ala His Leu Val Asp Asp Ala Tyr Ile Xaa Lys
 20 25 28

F.Y.I.
 →

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 04/17/2001

PATENT APPLICATION: US/09/446,089B

TIME: 13:33:08

Input Set : A:\001560-377.ST25.txt

Output Set: N:\CRF3\04172001\I446089B.raw

L:392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:441 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:456 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:481 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:496 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13